==
Sequence Listing was accepted.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2008; month=1; day=30; hr=12; min=5; sec=23; ms=105;]
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Application No: 10540431   Version No: 2.1

                   Input Set:

                   Output Set:

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                 Finished: 2008-01-30 12:03:24.765
                  Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 97 ms
           Total Warnings: 18
             Total Errors: 8
     No. of SeqIDs Defined: 18
        Actual SeqID Count: 18

Error code   Error Description

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W   213   Artificial or Unknown found in <213> in SEQ ID (2)

W   213   Artificial or Unknown found in <213> in SEQ ID (3)

W   213   Artificial or Unknown found in <213> in SEQ ID (4)

W   213   Artificial or Unknown found in <213> in SEQ ID (5)

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W   213   Artificial or Unknown found in <213> in SEQ ID (10)

W   213   Artificial or Unknown found in <213> in SEQ ID (11)

W   213   Artificial or Unknown found in <213> in SEQ ID (12)

W   213   Artificial or Unknown found in <213> in SEQ ID (13)

W   213   Artificial or Unknown found in <213> in SEQ ID (14)

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W   213   Artificial or Unknown found in <213> in SEQ ID (18)

E   257   Invalid sequence data feature in <221> in SEQ ID (18)

E   257   Invalid sequence data feature in <221> in SEQ ID (18)

Input Set:

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Error code	Error Description
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E 257	Invalid sequence data feature in <221> in SEQ ID (18)
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<110> KULSETH, MARI ANN

<120> PEPTIDES THAT BIND TO THE HEPARIN BINDING DOMAIN OF
      VEGF AND VEGFR-2

<130> PN0273

<140> 10540431
<141> 2005-06-22

<150> PCT/NO03/00444
<151> 2003-12-29

<150> NO 20026286
<151> 2002-12-30

<160> 18

<170> PatentIn Ver. 3.3

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<212> PRT
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<220>
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<220>
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<210> 3
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<210> 8
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<220>
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<220>
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Gly Cys
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  1               5                   10
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<222> (4)
<223> Tyr, Ser, Asn, Glu, Asp or Thr

<220>
<221> MOD_RES
<222> (5)
<223> Ala or Ser

<220>
<221> MOD_RES
<222> (8)
<223> Thr, Val, Met, Ser, Trp, Tyr, Leu or Ala

<220>
<221> MOD_RES
<222> (9)
<223> Tyr or Phe

<220>
<221> MOD_RES
<222> (11)
<223> Any amino acid residue capable of forming a
      disulphide bond, preferably a cysteine or a
      homocysteine residue or absent

<220>
<221> MOD_RES
<222> (12)..(21)
<223> Variable amino acid and this region may encompass
      0 to 10 residues

<220>
<223> See specification as filed for detailed description of
      substitutions and preferred embodiments

<400> 18
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  1               5                   10                  15

Xaa Xaa Xaa Xaa Xaa
            20
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